

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	3	PLAG1 and CTNNB1	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:37
L2	17	PLAG1	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:38
L3	50	CTNNB1 and (cancer\$3 tumor\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:38
L4	1	I3 and (CTNNB1 near5 fus\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:39
L5	1	(CTNNB1 near5 fus\$3)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:39
L6	21	(beta adj1 catenin) near5 fus\$3	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:40
L7	14	((beta adj1 catenin) CTNNB1) near5 (exon)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2005/06/15 18:41

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:54:54 ; Search time 30170 Seconds  
(without alignments)  
11745.210 Million cell updates/sec

Title: US-09-242-772-116  
Perfect score: 7313  
Sequence: 1 ggagcgcatatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7313	100.0	7313	9	HSU65002	U65002 Human zinc
2	7262	99.3	7313	6	A69511	A69511 Sequence 1
c 3	5728	78.3	142102	9	AC107952	AC107952 Homo sapi
4	1514	20.7	1565	9	BC075047	BC075047 Homo sapi
5	1514	20.7	1565	9	BC075048	BC075048 Homo sapi
6	687	9.4	65748	2	AC090187	AC090187 Homo sapi
7	601	8.2	49357	2	AC107961	AC107961 Homo sapi
c 8	420	5.7	65748	2	AC090187	AC090187 Homo sapi
c 9	406	5.6	421	11	G25280	G25280 human STS E

# Untitled

	10	381	5.2	550	9	AF221550	AF221550 Homo sapi
c	11	315	4.3	376	6	AR274991	AR274991 Sequence
	12	225	3.1	274	9	AF221549	AF221549 Homo sapi
c	13	177	2.4	177	11	G33002	G33002 A009Z02 Hum
	14	119	1.6	524	9	AF221548	AF221548 Homo sapi
	15	117	1.6	3161	10	AY574219	AY574219 Mus muscu
c	16	117	1.6	182102	2	AC097274	AC097274 Mus muscu
c	17	117	1.6	241148	10	AL807387	AL807387 Mouse DNA
c	18	110	1.5	49357	2	AC107961	AC107961 Homo sapi
	19	100	1.4	201	11	BV200913	BV200913 sqnm20538
	20	98	1.3	135	9	HSU78783	U78783 Human tumor
	21	80	1.1	278377	2	AC129839	AC129839 Rattus no
	22	78	1.1	1575	10	AF057366	AF057366 Mus muscu
c	23	66	0.9	244955	2	AC123210	AC123210 Rattus no
	24	60	0.8	60	6	CQ543597	CQ543597 Sequence
	25	50	0.7	1381	5	CR406846	CR406846 Gallus ga
c	26	45	0.6	66	11	HSU84997	U84997 Homo sapien
	27	39	0.5	107	5	CR353258	CR353258 Gallus ga
c	28	36	0.5	176067	10	AC129040	AC129040 Rattus no
c	29	36	0.5	185673	2	AC141142	AC141142 Rattus no
	30	35	0.5	660	6	AR502666	AR502666 Sequence
	31	35	0.5	660	6	AR517948	AR517948 Sequence
	32	35	0.5	160726	9	AC092421	AC092421 Homo sapi
	33	35	0.5	172947	2	AC068813	AC068813 Homo sapi
c	34	35	0.5	173037	2	AC018542	AC018542 Homo sapi
c	35	35	0.5	179190	9	AC114477	AC114477 Homo sapi
	36	35	0.5	194609	2	AC013775	AC013775 Mus muscu
	37	35	0.5	207086	10	AL596117	AL596117 Mouse DNA
	38	35	0.5	228232	2	AC090293	AC090293 Mus muscu
	39	34	0.5	728	10	BC031746	BC031746 Mus muscu
	40	34	0.5	752	8	AY125589	AY125589 Cyldindrot
	41	34	0.5	840	3	AY089459	AY089459 Drosophil
	42	34	0.5	1900	9	BC071628	BC071628 Homo sapi
	43	34	0.5	2192	5	BC063223	BC063223 Xenopus t
	44	34	0.5	3440	10	BC047268	BC047268 Mus muscu
	45	34	0.5	3911	8	AY639654	AY639654 Pinus rad

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:37:20 ; Search time 3456 Seconds  
(without alignments)  
12526.351 Million cell updates/sec

Title: US-09-242-772-116  
Perfect score: 7313  
Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7262	99.3	7313	2	AAV29268	Aav29268 Nucleotid
c 2	315	4.3	376	10	ADB31412	Adb31412 Testoster
3	117	1.6	4050	12	ADO35615	Ado35615 Novel mou
c 4	117	1.6	24348	11	ACN44976	Acn44976 Mouse gen
5	72	1.0	72	4	AAS13082	Aas13082 DNA encod
6	72	1.0	72	8	ACC41633	Acc41633 Human zin
7	60	0.8	60	6	ABN40484	Abn40484 Human spl
8	35	0.5	24127	11	ACN44540	Acn44540 Mouse gen
c 9	34	0.5	540	10	ABX57327	Abx57327 Arabidops
10	34	0.5	3463	3	AAA40241	Aaa40241 Pig heart

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	11	33	0.5	261	12	ADQ18288	Adq18288 Human sof
	12	33	0.5	330	12	ADQ20280	Adq20280 Human sof
c	13	33	0.5	360	6	ABQ85662	Abq85662 Arabidops
c	14	33	0.5	372	5	ABV37528	Abv37528 Human pro
c	15	33	0.5	385	10	ABX61502	Abx61502 Arabidops
	16	33	0.5	413	4	AAI85388	Aai85388 Human pol
	17	33	0.5	479	13	ACN52747	Acn52747 Cotton an
c	18	33	0.5	483	13	ACN47280	Acn47280 Cotton pr
	19	33	0.5	512	9	ACH26480	Ach26480 Human adu
	20	33	0.5	523	13	ACN58184	Acn58184 Cotton gy
	21	33	0.5	945	10	ADL18516	Adl18516 Rice glut
	22	33	0.5	1034	6	ABK65255	Abk65255 Arabidops
	23	33	0.5	1034	10	ADD29974	Add29974 Plant yie
	24	33	0.5	1034	12	ADI41806	Adi41806 Plant tra
	25	33	0.5	1335	3	AAA47331	Aaa47331 FtsZ homo
	26	33	0.5	1372	12	ADQ22819	Adq22819 Human sof
	27	33	0.5	1372	12	ADQ22824	Adq22824 Human sof
	28	33	0.5	1510	4	AAD08081	Aad08081 Rice oleo
	29	33	0.5	1832	5	ADL63631	Adl63631 Human ova
	30	33	0.5	2206	4	ABK43595	Abk43595 DNA encod
	31	33	0.5	2206	12	ADI53982	Adi53982 cDNA enco
	32	33	0.5	2385	4	ABL15036	Ab115036 Drosophil
c	33	33	0.5	2398	3	AAZ37263	Aaz37263 SGRF codi
	34	33	0.5	2540	6	ABQ73251	Abq73251 Human MAP
	35	33	0.5	2823	4	AAS34806	Aas34806 cDNA enco
	36	33	0.5	2823	10	ADC45964	Adc45964 Human neo
	37	33	0.5	8447	6	ABN80093	Abn80093 Human che
c	38	32	0.4	51	4	AAL28293	Aal28293 Human SNP
	39	32	0.4	163	5	ABV58311	Abv58311 Human pro
	40	32	0.4	204	5	ABV57555	Abv57555 Human pro
	41	32	0.4	312	5	ABV49552	Abv49552 Human pro
c	42	32	0.4	341	10	ABX61217	Abx61217 Arabidops
	43	32	0.4	348	4	AAI80658	Aai80658 Human pol
c	44	32	0.4	389	5	ABV61698	Abv61698 Human pro
	45	32	0.4	397	4	AAI86207	Aai86207 Human pol

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 04:06:47 ; Search time 3852 Seconds  
(without alignments)  
11784.990 Million cell updates/sec

Title: US-09-242-772-116  
Perfect score: 7313  
Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6054689 seqs, 3103772919 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12109378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	7313	100.0	7313	9	US-09-242-772-116	Sequence 116, App
c 2	315	4.3	376	21	US-10-831-704-128	Sequence 128, App
c 3	117	1.6	24348	13	US-10-087-192-1693	Sequence 1693, Ap
4	72	1.0	72	9	US-09-785-632A-136	Sequence 136, App
5	72	1.0	72	16	US-10-223-765-136	Sequence 136, App
6	60	0.8	60	10	US-09-908-975-13232	Sequence 13232, A
7	35	0.5	240	18	US-10-424-599-118528	Sequence 118528,
c 8	35	0.5	671	20	US-10-425-115-64671	Sequence 64671, A
9	35	0.5	735	20	US-10-425-115-17914	Sequence 17914, A
10	35	0.5	3112	20	US-10-425-115-51136	Sequence 51136, A
11	35	0.5	24127	13	US-10-087-192-1039	Sequence 1039, Ap
12	34	0.5	470	19	US-10-437-963-45935	Sequence 45935, A
c 13	34	0.5	540	9	US-09-770-152-679	Sequence 679, App
c 14	34	0.5	2124	18	US-10-424-599-3238	Sequence 3238, Ap
15	33	0.5	197	20	US-10-425-115-36720	Sequence 36720, A
16	33	0.5	261	20	US-10-723-860-1106	Sequence 1106, Ap
17	33	0.5	270	19	US-10-437-963-6529	Sequence 6529, Ap
18	33	0.5	282	20	US-10-425-115-134998	Sequence 134998,
19	33	0.5	330	20	US-10-723-860-3100	Sequence 3100, Ap
c 20	33	0.5	345	20	US-10-425-115-31440	Sequence 31440, A
c 21	33	0.5	360	9	US-09-770-791-532	Sequence 532, App
c 22	33	0.5	372	20	US-10-357-930-37547	Sequence 37547, A
23	33	0.5	375	20	US-10-425-115-165833	Sequence 165833,
24	33	0.5	380	20	US-10-425-115-57654	Sequence 57654, A
25	33	0.5	384	18	US-10-424-599-58174	Sequence 58174, A
c 26	33	0.5	385	9	US-09-924-035A-848	Sequence 848, App
c 27	33	0.5	392	20	US-10-425-115-65919	Sequence 65919, A
c 28	33	0.5	402	18	US-10-424-599-76918	Sequence 76918, A
29	33	0.5	422	20	US-10-425-115-89893	Sequence 89893, A
c 30	33	0.5	427	20	US-10-425-115-4382	Sequence 4382, Ap
31	33	0.5	430	20	US-10-425-115-58879	Sequence 58879, A
c 32	33	0.5	458	19	US-10-437-963-86639	Sequence 86639, A
c 33	33	0.5	465	19	US-10-437-963-34432	Sequence 34432, A
34	33	0.5	479	19	US-10-021-323-7528	Sequence 7528, Ap
c 35	33	0.5	483	19	US-10-021-323-2061	Sequence 2061, Ap
c 36	33	0.5	484	18	US-10-424-599-92471	Sequence 92471, A
37	33	0.5	512	10	US-09-918-995-13692	Sequence 13692, A
38	33	0.5	523	19	US-10-021-323-12965	Sequence 12965, A
c 39	33	0.5	570	20	US-10-425-115-48090	Sequence 48090, A
c 40	33	0.5	626	20	US-10-425-115-14398	Sequence 14398, A
c 41	33	0.5	637	20	US-10-425-115-33996	Sequence 33996, A
c 42	33	0.5	690	20	US-10-425-115-164109	Sequence 164109,
43	33	0.5	715	21	US-10-956-157-3705	Sequence 3705, Ap
44	33	0.5	715	21	US-10-956-157-8940	Sequence 8940, Ap
c 45	33	0.5	787	20	US-10-425-115-126784	Sequence 126784,

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 01:23:31 ; Search time 3482 Seconds  
(without alignments)  
9277.886 Million cell updates/sec

Title: US-09-242-772-116  
Perfect score: 7313  
Sequence: 1 ggcagcgcatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 12999316 seqs, 2208778887 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25998632

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq2:\*  
3: /cgn2\_6/ptodata/2/pna/US06\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US07\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US08\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US09\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq:\*  
8: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq2:\*  
9: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq3:\*  
10: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq4:\*  
11: /cgn2\_6/ptodata/2/pna/US10\_NEW\_COMB.seq5:\*  
12: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq:\*  
13: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq2:\*  
14: /cgn2\_6/ptodata/2/pna/US11\_NEW\_COMB.seq3:\*  
15: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	563	7.7	4174	15	US-60-680-544-32916	Sequence 32916, A
2	563	7.7	4174	15	US-60-680-473-32916	Sequence 32916, A
3	35	0.5	760	9	US-10-703-032-103073	Sequence 103073,
c 4	34	0.5	601	11	US-10-940-774A-28962	Sequence 28962, A
c 5	34	0.5	601	11	US-10-940-774A-125909	Sequence 125909,
c 6	34	0.5	115963	11	US-10-940-774A-12298	Sequence 12298, A
c 7	34	0.5	144322	11	US-10-940-774A-15316	Sequence 15316, A
c 8	34	0.5	152321	15	US-60-659-397-12128	Sequence 12128, A



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c	9	33	0.5	201	11	US-10-990-328A-541037	Sequence 541037,
	10	33	0.5	400	9	US-10-703-032-73280	Sequence 73280, A
c	11	33	0.5	400	9	US-10-703-032-99398	Sequence 99398, A
	12	33	0.5	450	9	US-10-703-032-79323	Sequence 79323, A
c	13	33	0.5	456	9	US-10-703-032-70659	Sequence 70659, A
c	14	33	0.5	496	9	US-10-703-032-88434	Sequence 88434, A
c	15	33	0.5	601	11	US-10-940-774A-115142	Sequence 115142,
c	16	33	0.5	696	9	US-10-703-032-13726	Sequence 13726, A
c	17	33	0.5	732	9	US-10-703-032-12833	Sequence 12833, A
c	18	33	0.5	766	9	US-10-703-032-17311	Sequence 17311, A
	19	33	0.5	1034	6	US-09-713-994A-1780	Sequence 1780, Ap
	20	33	0.5	1747	7	US-10-062-254A-357	Sequence 357, App
	21	33	0.5	2385	12	US-11-097-143-19795	Sequence 19795, A
	22	33	0.5	11730	11	US-10-940-774A-14991	Sequence 14991, A
	23	33	0.5	29571	15	US-60-659-397-12103	Sequence 12103, A
c	24	33	0.5	49416	11	US-10-940-774A-15234	Sequence 15234, A
c	25	33	0.5	93364	11	US-10-940-774A-14890	Sequence 14890, A
	26	33	0.5	151541	11	US-10-990-328A-97855	Sequence 97855, A
	27	33	0.5	283538	11	US-10-940-774A-13506	Sequence 13506, A
	28	33	0.5	401433	2	PCT-US04-42189-79	Sequence 79, App1
c	29	33	0.5	474412	11	US-10-990-328A-98016	Sequence 98016, A
	30	33	0.5	483207	1	PCT-US04-37982-3303	Sequence 3303, Ap
c	31	32	0.4	51	6	US-09-749-280D-1501	Sequence 1501, Ap
c	32	32	0.4	201	11	US-10-990-328A-215196	Sequence 215196,
c	33	32	0.4	201	11	US-10-990-328A-215230	Sequence 215230,
	34	32	0.4	201	11	US-10-990-328A-234783	Sequence 234783,
	35	32	0.4	201	11	US-10-990-328A-234784	Sequence 234784,
	36	32	0.4	446	9	US-10-703-032-3773	Sequence 3773, Ap
c	37	32	0.4	525	15	US-60-680-544-3950	Sequence 3950, Ap
	38	32	0.4	525	15	US-60-680-544-14578	Sequence 14578, A
c	39	32	0.4	525	15	US-60-680-473-3950	Sequence 3950, Ap
	40	32	0.4	525	15	US-60-680-473-14578	Sequence 14578, A
	41	32	0.4	564	9	US-10-703-032-57200	Sequence 57200, A
	42	32	0.4	600	13	US-11-060-756-278	Sequence 278, App
	43	32	0.4	600	13	US-11-060-756-4550	Sequence 4550, Ap
	44	32	0.4	784	7	US-10-456-882A-40	Sequence 40, App1
	45	32	0.4	830	15	US-60-680-544-17295	Sequence 17295, A

# Untitled

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OM nucleic - nucleic search, using sw model

Run on: June 20, 2005, 11:48:05 ; Search time 21091 Seconds  
(without alignments)  
13198.236 Million cell updates/sec

Title: US-09-242-772-116  
Perfect score: 7313  
Sequence: 1 ggagcgcatatacactacaat.....tatgaataaaatctcgtgcc 7313

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1452	19.9	1503	9	AY420150	AY420150 Homo sapi
2	685	9.4	693	4	BM724590	BM724590 UI-E-E01-
3	679	9.3	1503	9	AY420151	AY420151 Pan trogl
c 4	637	8.7	742	6	CA413047	CA413047 UI-H-EZ0-
5	596	8.1	864	5	BX370812	BX370812 BX370812
6	583	8.0	583	5	BP317766	BP317766 BP317766
c 7	570	7.8	570	2	AW339499	AW339499 xz91g05.x
c 8	548	7.5	734	6	CA411972	CA411972 UI-H-EZ0-
c 9	541	7.4	616	5	BU686683	BU686683 UI-CF-DU1
c 10	540	7.4	540	1	AA706806	AA706806 zj30c09.s
c 11	518	7.1	518	2	BF115791	BF115791 7n64h11.x
12	514	7.0	1047	5	BX402039	BX402039 BX402039
13	497	6.8	500	2	BF507694	BF507694 UI-H-BW1-
14	497	6.8	736	1	AL036879	AL036879 DKFZp564P

# Untitled

	15	487	6.7	1165	5	BX424854	BX424854
c	16	482	6.6	482	1	AA707386	AA707386 zj27e09.s
	17	475	6.5	790	1	AU138448	AU138448 AU138448
c	18	464	6.3	466	1	AA628501	AA628501 af27d06.s
	19	461	6.3	909	5	BU181917	BU181917 AGENCOURT
c	20	459	6.3	467	2	AW274762	AW274762 xn34h01.x
c	21	448	6.1	597	2	AW977860	AW977860 EST389864
	22	439	6.0	449	6	CA771364	CA771364 io70c07.y
	23	438	6.0	907	4	BG613583	BG613583 602641935
c	24	430	5.9	432	2	BF432133	BF432133 nab79g01.
	25	426	5.8	536	7	CN410058	CN410058 170004245
c	26	423	5.8	423	1	AI334157	AI334157 qq07h12.x
c	27	409	5.6	458	2	AW002999	AW002999 wq62d08.x
c	28	409	5.6	560	1	AI808840	AI808840 wf97h04.x
c	29	406	5.6	421	7	D59273	D59273 HUM007A10A
c	30	373	5.1	373	1	AA418372	AA418372 zv96g12.r
c	31	373	5.1	494	2	AW007402	AW007402 wt55b04.x
	32	371	5.1	569	5	BP379355	BP379355 BP379355
c	33	353	4.8	427	1	AI223324	AI223324 qg71c02.x
c	34	347	4.7	391	7	N95376	N95376 zb71f10.s1
	35	320	4.4	460	1	AV745206	AV745206 AV745206
c	36	315	4.3	673	9	AG120959	AG120959 Pan trogl
	37	310	4.2	514	7	CN410057	CN410057 170005830
	38	305	4.2	467	7	T83418	T83418 yd44d05.r1
	39	299	4.1	410	7	CN410056	CN410056 170005325
	40	288	3.9	319	2	AW138020	AW138020 UI-H-BI1-
c	41	285	3.9	517	7	T81600	T81600 yd44d05.s1
	42	284	3.9	489	1	AV745506	AV745506 AV745506
	43	261	3.6	454	1	AA418251	AA418251 zv96c12.s
	44	259	3.5	259	1	AA421591	AA421591 zu25f01.r
	45	249	3.4	922	4	BG253502	BG253502 602364227